

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 12, 2005, 00:18:59 ; Search time 3598 Seconds  
(without alignments)  
2578.424 Million cell updates/sec

Title: US-09-982-091a-4  
Perfect score: 6836  
Sequence: 1 MTBEVSGSVHLEINDEPNVIS.....LTMSGAPIPGFFLSPDPHG 1332

Scoring table:  
BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 8443130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 1686260

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Command line parameters:

-MODE=frame+ p2n.model -DEV=xlh  
-O=/cgnt1/USPTO.epool/US09982091/rnatc.1102005.162446.21223/app.query.fasta\_1.1479  
-DB=Published Applications NA -OPT=fastap -SUPER=ep2n.rnpb -MINMATCH=0.1  
-LOPCU=0 -LOPEXT=0 -UNIT=bits -START=1 -END=-1 -MATRIX=blowum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pcr -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -USER=US09982091 @CGN 1.1.1287 @rnatc.1102005.162446.21223  
-NCPU=6 -ICPU=3 -NO MAP -LARGESUBSTR -NEG SCORES=0 -MAIT -DSBLOCK=100  
-LONGLOG -DEV TIMEOUT=130 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FAPOP=6 -FAPEXT=7 -YAPOP=10 -YAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

Published Applications NA:\*

- 1: /cgnt2\_6/prodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgnt2\_6/prodata/1/pubpna/US09\_PCT\_NEW\_PUB.seq:\*
- 3: /cgnt2\_6/prodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgnt2\_6/prodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 5: /cgnt2\_6/prodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 6: /cgnt2\_6/prodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 7: /cgnt2\_6/prodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 8: /cgnt2\_6/prodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 9: /cgnt2\_6/prodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 10: /cgnt2\_6/prodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgnt2\_6/prodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 12: /cgnt2\_6/prodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 13: /cgnt2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 14: /cgnt2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 15: /cgnt2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 16: /cgnt2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 17: /cgnt2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 18: /cgnt2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 19: /cgnt2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 20: /cgnt2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 21: /cgnt2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 22: /cgnt2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 23: /cgnt2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 24: /cgnt2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 25: /cgnt2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 26: /cgnt2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6836	100.0	4756	9 US-09-982-091A-3	Sequence 3, Appl1
2	6822	99.8	4804	20 US-10-357-930-30217	Sequence 30217, A
3	2687	39.3	4754	9 US-09-982-091A-1	Sequence 1, Appl1
4	2019	29.5	58837	9 US-09-982-091A-5	Sequence 5, Appl1
5	850	12.4	511	15 US-10-106-698-1296	Sequence 1256, Ap
6	813	11.9	111206	13 US-10-087-192-1957	Sequence 1957, Ap
7	763	11.2	11547	9 US-09-988-598-480	Sequence 480, App
8	697	10.2	5439	24 US-11-097-143-857	Sequence 857, App
9	656	9.6	484	9 US-09-998-598-268	Sequence 268, App
10	610	9.3	496	10 US-09-918-995-21694	Sequence 21694, A
11	610	8.9	421	10 US-09-803-719-1138	Sequence 1138, Ap
12	606	8.9	9315	24 US-11-097-143-856	Sequence 856, App
13	554	8.1	422	10 US-09-803-719-1139	Sequence 1139, Ap
14	544	8.0	452	20 US-10-357-930-45120	Sequence 45720, A
15	523	7.7	401	20 US-10-357-930-15892	Sequence 15892, A
16	508	7.4	393	10 US-09-803-719-853	Sequence 853, App
17	500	7.3	408	10 US-09-803-719-777	Sequence 777, App
18	416	6.1	473	20 US-10-357-930-46021	Sequence 46021, A
19	400.5	5.9	24789	24 US-11-097-143-40201	Sequence 40201, A
20	390	5.7	18506	24 US-11-097-143-5629	Sequence 5629, Ap
21	388.5	5.7	7568	22 US-10-450-763-16627	Sequence 16627, A
22	388.5	5.7	9161	17 US-10-133-937-37	Sequence 37, Appl
23	388.5	5.7	9161	17 US-10-159-563-37	Sequence 37, Appl
24	388.5	5.7	9220	20 US-10-357-930-24403	Sequence 24403, A
25	388.5	5.7	9220	20 US-10-357-930-25254	Sequence 25254, A
26	388.5	5.7	9416	19 US-10-755-888-614	Sequence 614, App
27	388.5	5.7	9416	21 US-10-489-740-114	Sequence 114, App
28	388.5	5.7	11957	22 US-10-765-700-32	Sequence 32, Appl
29	388.5	5.7	11957	22 US-10-252-157-218	Sequence 218, Appl
30	382.5	5.6	4380	17 US-10-094-466-29	Sequence 29, Appl
31	376.5	5.5	7095	18 US-10-205-351-67	Sequence 67, Appl
32	367	5.4	6607	10 US-09-814-331-19998	Sequence 19998, A
33	367	5.4	6616	20 US-10-357-930-23673	Sequence 23673, A
34	366.5	5.4	5311	9 US-09-764-176-6	Sequence 6, Appl1
35	359.5	5.3	5040	17 US-10-369-493-45767	Sequence 45767, A
36	355.5	5.2	4721	24 US-11-097-143-29150	Sequence 29150, A
37	354	5.2	8307	24 US-11-097-143-31982	Sequence 31982, A
38	354	5.2	11030	21 US-10-956-157-426	Sequence 426, App
39	353.5	5.2	10330	22 US-10-934-998-25	Sequence 25, Appl
40	353.5	5.2	10452	11 US-09-968-007A-490	Sequence 490, App
41	353.5	5.2	10452	21 US-10-843-641A-6860	Sequence 6860, App
42	353.5	5.2	10452	22 US-10-934-998-50	Sequence 50, Appl
43	353.5	5.2	11167	16 US-10-252-157-188	Sequence 188, Appl
44	353.5	5.2	422	20 US-10-357-930-16195	Sequence 16195, A
45	353	5.2			

## ALIGNMENTS

RESULT 1  
US-09-982-091A-3  
Sequence 3, Application US/09982091A  
Patent No. US20020151030A1  
GENERAL INFORMATION:  
APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY  
APPLICANT: KIMAGAI, Akiko  
APPLICANT: DUNPHY, William  
TITLE OF INVENTION: CLASPIN PROTEINS AND METHODS OF USE THEREOF  
FILE REFERENCE: CIT3320-1  
CURRENT APPLICATION NUMBER: US/09/982,091A  
CURRENT FILING DATE: 2002-10-17  
PRIOR APPLICATION NUMBER: US 60/241,246  
PRIOR FILING DATE: 2000-10-17  
NUMBER OF SEQ IDS NOS: 12  
SOFTWARE: PatentIn version 3.1

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_p2n model

Run on: October 11, 2005, 19:40:24 ; Search time 704 Seconds  
(without alignments)  
3095.910 Million cell updates/sec

Title: US-09-982-091A-4  
Perfect score: 6836  
Sequence: 1 MTGEGVSEVHLKINDPVIS.....LTMSGAPIPGRFSLPDPHG 1332

Scoring table:

BLASTN62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+g2n.model -DEV=xlh  
-Q/cg2n1/USPTO.spool/US09982091/runat 1102005 162444 21143/app query.fasta\_1.1479  
-DB=Issued\_Patents\_NA -OPMT=fastap -SUFFIX=g2n.rn1 -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNIT=512s -START=1 -END=-1 -MATRIX=blomsum2 -TRANS=human40.cdd  
-LIST=45 -DOCALLIGN=200 -THR SCORE=Pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pct -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USRR=US09982091.OCGN.1.1.302/runat 1102005 162444 21143 -NCPV=6 -ICPV=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-NO TIMEOUT=120 -MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued\_Patents\_NA.\*

1: /cg2n\_6/ptodata/1/ina/5A.COMB.seq.\*  
2: /cg2n\_6/ptodata/1/ina/5B.COMB.seq.\*  
3: /cg2n\_6/ptodata/1/ina/6A.COMB.seq.\*  
4: /cg2n\_6/ptodata/1/ina/6B.COMB.seq.\*  
5: /cg2n\_6/ptodata/1/ina/PCTUS.COMB.seq.\*  
6: /cg2n\_6/ptodata/1/ina/backfillseq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6792.5	99.4	4756	US-09-949-016-4455	Sequence 4455, Ap
2	1988.5	29.1	53737	US-09-949-016-16197	Sequence 16197, A
3	416	6.1	601	US-09-949-016-159256	Sequence 159256, A
4	388.5	5.7	7571	US-09-949-016-4366	Sequence 4366, Ap
5	388.5	5.7	8146	US-09-976-594-725	Sequence 725, App
6	388.5	5.7	11917	US-09-566-921-32	Sequence 93, Appl
7	388.5	5.7	101300	US-09-949-016-16108	Sequence 16108, A
8	382	5.6	9551	US-08-056-200-93	Sequence 93, Appl
9	376	5.5	11236	US-07-853-913-1	Sequence 1, Appl
10	366.5	5.4	5331	US-09-764-176-6	Sequence 6, Appl
11	350	5.1	6755	US-08-931-999-4	Sequence 4, Appl

13	348	5.1	10300	US-09-949-016-636	Sequence 636, App
14	344.5	5.0	8590	US-09-949-016-5562	Sequence 5562, Ap
15	341	5.0	38575	US-09-949-016-17304	Sequence 17304, A
16	341	5.0	119153	US-09-949-016-12378	Sequence 12378, A
17	327	4.8	9626	US-09-150-867-2	Sequence 2, Appl
18	313	4.6	8503	US-09-620-312D-130	Sequence 130, App
19	312	4.6	5361	US-08-973-462-2	Sequence 2, Appl
20	312	4.6	6152	US-08-973-462-1	Sequence 1, Appl
21	311.5	4.6	6008	US-09-949-016-5058	Sequence 5058, Ap
22	311	4.5	3489	US-08-728-323A-1	Sequence 1, Appl
23	311	4.5	3489	US-09-298-568-1	Sequence 1, Appl
24	311	4.5	3489	US-09-410-399-1	Sequence 1, Appl
25	311	4.5	3489	US-09-894-273-1	Sequence 1, Appl
26	311	4.5	32207	US-08-770-379-20	Sequence 20, Appl
27	311	4.5	32207	US-08-757-669A-20	Sequence 20, Appl
28	311	4.5	32207	US-09-230-371A-20	Sequence 20, Appl
29	308	4.5	8257	US-09-595-684B-30	Sequence 30, Appl
30	307	4.5	6861	US-09-949-016-1240	Sequence 1240, Ap
31	307	4.5	6861	US-09-949-016-1241	Sequence 1241, Ap
32	307	4.5	6861	US-09-949-016-1242	Sequence 1242, Ap
33	306.5	4.5	5883	US-09-949-016-5001	Sequence 5001, Ap
34	306	4.5	5661	US-08-938-105-2	Sequence 2, Appl
35	305.5	4.5	5574	US-09-917-254-40	Sequence 40, Appl
36	303	4.4	6175	US-08-875-435B-1	Sequence 1, Appl
37	302.5	4.4	7596	US-09-023-655-1463	Sequence 1463, Ap
38	302	4.4	11091	US-09-134-001C-2243	Sequence 2243, Ap
39	301	4.4	7585	US-09-418-710-22	Sequence 22, Appl
40	301	4.4	7585	US-09-839-479-22	Sequence 22, Appl
41	300.5	4.4	8587	US-09-220-132-79	Sequence 79, Appl
42	299.5	4.4	6016	US-09-949-016-2264	Sequence 26, Ap
43	299.5	4.4	8560	US-09-949-016-1788	Sequence 1788, Ap
44	299.5	4.4	8560	US-09-949-016-1789	Sequence 1789, Ap
45	299	4.4	6158	US-09-799-451-897	Sequence 897, App

# ALIGNMENTS

RESULT 1  
US-09-949-016-4455  
Sequence 4455, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: CLO01307  
CURRENT APPLICATION NUMBER: US/09/949, 016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 4455  
LENGTH: 4756  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-4455  
Alignment Scores:  
Pred. No.: 0  
Score: 6792.50  
Percent Similarity: 99.63%  
Best Local Similarity: 99.63%  
Query Match: 99.36%  
DB: 4  
Gaps: 1  
US-09-982-091A-4 (1-1332) x US-09-949-016-4455 (1-4756)  
OY 1 MetThciGyUvAlGtYSerGtUvAlHtLeGtUvAlLeaBnApPtoAnVAlIleSer 20

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

# OM protein - nucleic search, using frame\_plus.p2n model

Run on: October 11, 2005, 19:39:09 ; Search time 9226 Seconds  
(without alignments) 5495.513 Million cell updates/sec

Title: US-09-982-091A-4

Perfect score: 6836

Sequence: 1 MTGEVSEVHLEINDPVIS.....LTWSGAPPGFRLSPDPRG 1332

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Command line parameters:

-MODE=frame+ .p2n.model -DEV=xlh  
-O=/cgrt\_1/USPTO.spool/US09982091/runac\_11102005.162443.21129/app\_query.fasta\_1.1479  
-DB=EST -QPM=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOFC=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pcr -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ps -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09982091 @CGEN 1.1 7037 @runac\_11102005.162443.21129 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONCLOG  
-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6  
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELop=6 -DELEXT=7

## Database :

EST: +  
1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_hic.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_gse1.\*  
9: gb\_gse2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3319	48.6	2075	3	BC018670 Homo sapi
2	2101.5	30.7	2063	3	AK053847 Mus muscu
3	1494	21.9	1027	3	BQ072224 AGENCOURT
4	1324	19.4	930	4	BM461846 AGENCOURT
5	1324	19.4	883	5	BU193221 AGENCOURT
6	1302	19.0	823	5	BG469801 602534321
7	1246	18.2	883	5	BU181027 AGENCOURT
8	1186.5	17.4	929	5	BQ963412 AGENCOURT
9	1135.5	16.6	751	7	CF749459 UT-M-HD0

10	1133	16.6	594	4	BM676972	UT-E-B01-
11	1116.5	16.3	943	4	BP968339	BP968339 602269405
12	1111	16.3	942	2	BE882484	BE882484 601507224
13	1096	16.0	794	7	CF739118	CF739118 UT-M-HD0
14	1071	15.7	656	5	BU662956	BU662956 C193f06.z
15	1055	15.4	1166	5	BM907939	BM907939 AGENCOURT
16	1044	15.3	743	7	CF738075	CF738075 UT-M-HD0
17	1041	15.2	785	7	CNS28793	CNS28793 UT-M-HD0
18	1019	14.9	647	4	BM720876	BM720876 UT-E-B01-
19	1015	14.8	700	7	CK635361	CK635361 UT-M-HD0
20	1004	14.7	898	5	BQ227287	BQ227287 AGENCOURT
21	1003	14.7	869	5	BP166258	BP166258 BP166258
22	1001	14.6	582	5	BP279746	BP279746 BP279746
23	1001	14.6	582	5	BP279788	BP279788 BP279788
24	999	14.6	582	5	CF737000	CF737000 UT-M-HD0
25	990	14.5	786	7	BP313518	BP313518 BP313518
26	987.5	14.4	720	6	CD578928	CD578928 UT-M-FY0
27	961.5	14.1	630	7	CF724962	CF724962 UT-M-GZ0
28	956	14.0	595	7	CN309667	CN309667 170005326
29	950.5	13.9	691	7	CF748227	CF748227 UT-M-HD0
30	910	13.3	786	4	BI853368	BI853368 603379950
31	909	13.3	639	7	CF914774	CF914774 B0969A05-
32	907	13.3	529	4	BM799186	BM799186 K-EST0082
33	896.5	13.1	746	4	BG166364	BG166364 602345596
34	891	13.0	853	7	CR585850	CR585850 CR585850
35	881	12.9	513	4	BM828080	BM828080 K-EST0100
36	876	12.8	615	7	CF172511	CF172511 B0908E12-
37	866	12.7	570	6	CA536822	CA536822 C0239B04
38	855	12.5	583	5	BP363381	BP363381 BP363381
39	854	12.5	611	7	CF172978	CF172978 B0916H04
40	835	12.2	621	5	BO560356	BO560356 HA063G11-
41	827	12.1	582	5	BP221815	BP221815 BP221815
42	827	12.1	707	7	CN458990	CN458990 UT-M-HD0
43	822	12.0	494	1	A1569660	A1569660 t040b07.x
44	817.5	12.0	961	6	CA983046	CA983046 AGENCOURT
45	809	11.8	480	1	AA857451	AA857451 0103d08.s

## ALIGNMENTS

RESULT 1	BC018670	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS
BC018670	BC018670	BC018670	Homo sapiens claspain homolog (Xenopus laevis), mRNA (cDNA clone IMAGE:4104653), containing frame-shift errors.	BC018670	BC018670.1	GI:17391474	HTC	Homo sapiens (human)	1 (bases 1 to 2075)	Strausberg, R.L., Peinold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, P.S., Wagner, L., Shermen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Bietow, K.H., Schaefer, C.F., Bhac, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uddin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loggellano, N.A., Peters, G.J., Adams, R.D., Mullany, S.J., Bosak, S.A., McGowan, P.U., McKernan, K.J., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Young, A.C., Shcherchenko, Y., Sanchez, A., Whiting, M., Madan, A., Rodriguez, S., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalski, U., Smalhus, D.E., Scherck, A., Schein, J.E., Jones, S.J., Jones, S.J., and Marra, M.A.
TITLE	human and mouse cDNA sequences		human and mouse cDNA sequences							

Result No.	Score	Query Match	Length	DB	ID	Description
1	6836	100.0	4755	5	ABK52611	Abk52611 DNA encod
2	6822	99.8	4804	5	ABV03199	Abv03199 Human pro
3	6812	99.6	4414	10	ADG30694	Adg30694 Human no
4	2687	39.3	4754	6	ABK52610	Abk52610 DNA encod
5	2019	29.5	58837	6	ABK52612	Abk52612 Human Cla

6	850	12.4	511	4	AAH34164	Aah34164 Human col
7	813	11.9	111206	11	ACNA45152	Acrn45152 Mouse gen
8	780	11.4	1225	6	ABQ77931	Abq77931 Human mac
9	763	11.2	547	6	ABU87169	Abu87169 Human col
10	697	10.2	5339	4	ABE02411	ABE02411 Drosophi
11	656	9.6	484	6	ABV86957	ABv86957 Human col
12	635	9.3	496	6	ACH34482	Ach34482 Human end
13	610	8.9	421	4	AAH38080	Aah38080 Novel hum
14	606	8.9	9315	4	ABJ02410	ABj02410 Drosophi
15	554	8.1	422	4	AAH38081	Aah38081 Novel hum
16	544	8.0	452	5	ABV45701	ABv45701 Human pro
17	536	7.8	411	5	AAH66638	Aah66638 Novel hum
18	521	7.8	406	5	AAH66639	Aah66639 Novel hum
19	523	7.7	401	5	ABV15501	ABv15501 Human pro
20	508	7.4	393	4	AAH37795	Aah37795 Novel hum
21	504	7.4	300	2	AAZ12683	Aaz12683 Human gen
22	500	7.3	408	4	AAH37719	Aah37719 Novel hum
23	440	6.4	386	5	AAH64422	Aah64422 Novel hum
24	419	6.1	381	5	AAH64459	Aah64459 Novel hum
25	416	6.1	473	5	ABV46002	ABv46002 Human pro
26	401	5.9	298	2	AAZ12714	Aaz12714 Human gen
27	400.5	5.9	24789	4	ABJ28640	ABj28640 Drosophi
28	390	5.7	18506	4	ABJ05592	ABj05592 Drosophi
29	388.5	5.7	7568	5	AAH58023	Aah58023 DNA encod
30	388.5	5.7	8146	12	ADL12996	Adl12996 Human ste
31	388.5	5.7	9220	5	ABW24414	ABw24414 Human pro
32	388.5	5.7	9220	5	ABW25665	ABw25665 Human pro
33	388.5	5.7	9416	6	ABK83800	ABk83800 Human CDN
34	388.5	5.7	9416	8	ACF34559	Acf34559 Gene enco
35	388.5	5.7	9416	12	ADNO5259	Adno5259 Ant ipso
36	388.5	5.7	9416	13	ADRI4613	Adri4613 Human NF
37	388.5	5.7	11917	12	ADRI61664	Adri61664 Human CDN
38	388.5	5.7	11950	10	ADH53871	Adh53871 Human he
39	388.5	5.7	11965	10	ADH90735	Adh90735 Human he
40	388.5	5.7	12004	12	ADNO4560	Adno4560 Ant ipso
41	382.5	5.6	4380	6	ABH78735	ABh78735 DNA encod
42	382	5.6	9951	6	AAZ22301	AAz22301 CDNA enco
43	378	5.5	4755	13	ACN31449	ACn31449 Tumour-as
44	376.5	5.5	7095	9	ACD25360	ACd25360 Rat micro
45	376	5.5	5946	2	ADQ28398	ADq28398 Rat nesti

5	2687	39.3	4754	5	AF297867	AF297867 Xenopus	1
6	2473.5	36.2	111862	2	AL139143	AL139143 Homo sapi	
7	2019	29.5	194296	6	ALJ354864	ALJ354864 Human DNA	
8	1846.5	27.0	1093	6	CQ727305	CQ727305 Sequence	
9	1618.5	23.7	1751	10	AY324187	AY324187 Mus muscu	
10	1079.5	15.8	668	6	CQ727303	CQ727303 Sequence	
11	934.5	13.7	213391	10	AL606935	AL606935 Mouse DNA	
12	879	12.9	111862	2	AL139143	AL139143 Homo sapi	
13	865.5	11.7	223363	2	AC129700	AC129700 Rattus no	
14	813	11.9	190338	10	AC139216	AC139216 Mus muscu	
15	700	10.2	2230	3	AK174670	AK174670 Clona int	
16	697	10.2	5439	6	CQ573099	CQ573099 Sequence	
17	645.5	9.4	343858	2	AC095880	AC095880 Rattus no	
18	619	9.1	92047	10	AY135690	AY135690 Mus muscu	
19	610	8.9	421	6	AX246208	AX246208 Sequence	
20	606	8.9	9315	6	CQ573098	CQ573098 Sequence	
21	606	8.9	191335	2	AC010700	AC010700 Drosophi1	
22	606	8.9	210663	2	AC019525	AC019525 Drosophi1	
23	605	8.9	315988	3	AB003481	AB003481 Drosophi1	
24	595	8.7	247462	2	AC134478	AC134478 Rattus no	
25	554	8.1	422	6	AX246209	AX246209 Sequence	
26	549.5	8.0	203980	2	AC134058	AC134058 Rattus no	
27	544	8.0	452	6	CO513853	CO513853 Sequence	
28	536	7.8	411	6	AX071992	AX071992 Sequence	
29	531	7.8	406	6	AX071923	AX071923 Sequence	
30	523	7.7	401	6	CR484025	CR484025 Sequence	
31	523	7.7	1044	5	CR761574	CR761574 Xenopus t	
32	508	7.4	393	6	AX245923	AX245923 Sequence	
33	504	7.4	300	6	BD212010	BD212010 Novel hum	
34	500	7.3	408	6	AX245847	AX245847 Sequence	
35	497	7.1	418	9	BC062215	BC062215 Homo sapi	
36	487.5	7.1	160827	3	AC099025	AC099025 Drosophi1	
37	487.5	7.1	193262	3	AC007579	AC007579 Drosophi1	
38	487.5	7.1	260367	3	AB003808	AB003808 Drosophi1	
39	454	6.6	73391	8	AP002057	AP002057 Arabidops	
40	448	6.6	2243	9	AY113649	AY113649 Drosophi1	
41	447	6.5	206454	9	AC018737	AC018737 Homo sapi	
42	440	6.4	386	6	AX069706	AX069706 Sequence	
43	432	6.3	179145	9	AC009785	AC009785 Homo sapi	
44	431	6.3	68727	3	AC004516	AC004516 Drosophi1	
45	428.5	6.3	71023	2	AC004426	AC004426 Drosophi1	

RESULT 1

AF297866

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

ALIGNMENTS

4756 bp

mRNA

linear

PRI 21-OCT-2000

AF297866

Homo sapiens Hu-Claaspin mRNA, complete cds.

AF297866

AF297866.1 GI:10944333

Homo sapiens (human)

Homo sapiens

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.

1 (bases 1 to 4756)

Kumagai, A. and Dunphy, W.G.

Claaspin, a novel protein requized for the activation of Cdk1 during a DNA replication checkpoint response in Xenopus egg extracts

Mol. Cell 6 (4), 839-849 (2000)

2 (bases 1 to 4756)

Kumagai, A. and Dunphy, W.G.

Direct Submmission

Submitted (21-OUG-2000) Biology, California Institute of Technology, 1200 E. California Blvd., Pasadena, CA 91125, USA

Location/Qualifiers

1..4756

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"